## SEQUENCE LISTING

| <110> | MERCK-SANTE |          |    |    |           |              |        |  |
|-------|-------------|----------|----|----|-----------|--------------|--------|--|
|       | CENTRE      | NATIONAL | DE | LA | RECHERCHE | SCIENTIFIQUE | (CNRS) |  |

<120> Insulin-induced gene as therapeutic target in diabetes

<130> BFF 03P0004

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 1062

<212> DNA

<213> Rattus sp.

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gacttgtctg gtaaccccaa gctcaagtgg gcaggagccg aggtatttc aggcctgggt 840

ttgctgcaag aactagacct gtctggctcc agcctggtgc ccctgcctga gacgctgcta 900

catcacctcc ctgctttaca gagtgtcagt gtaggccaag atgtgcagtg ccggcgtctg 960

gtacgggagg gtgcctacca ccgccaaccc ggttccagcc ctaaggtagt cctgcactgt 1020

ggagacaccc aggaatctgc caggggcca gacatcttgt ga 1062

<210> 2

<211> 353

<212> PRT

<213> Rattus sp.

<400> 2

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Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Glu Glu Thr Phe 20 25 30

Gly Leu Phe Asp Ser Phe Ser Leu Ile Arg Val Asp Cys Ser Ser Leu  $35 \hspace{1cm} 40 \hspace{1cm} 45$ 

Gly Pro His Ile Val Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu 50 55 60

Asp Leu Ser Ser Asn Arg Leu Glu Thr Val Asn Glu Ser Val Leu Gly 65 70 75 80

Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu 85 90 95

Leu Thr Ser Ile Thr Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu  $100 \hspace{1cm} 105 \hspace{1cm} 110$ 

Ser Leu Asp Leu Ser His Asn Gly Leu Ala Ala Leu Pro Ala Glu Val 115 120 125

Phe Thr Ser Ser Pro Leu Ser Asp Ile Asn Leu Ser His Asn Arg Leu 130 135 140

Arg Glu Val Ser Ile Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala 145 150 155 160

Leu His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Leu Pro Tyr 165 170 175

Pro Ala Arg Ala Ser Leu Ser Ala Pro Thr Ile Gln Ser Leu Asn Leu 180 185 190

Ser Trp Asn Arg Leu Arg Ala Val Pro Asp Leu Arg Asp Leu Pro Leu 195 200 205

Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Thr Ile Asn Pro Gly 210 215 220

Gln Gly Ile Leu Gln Leu Pro Pro His Gly Phe Arg Glu Leu Pro Gly 245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Lys Trp Ala Gly 260 265 270

Ala Glu Val Phe Ser Gly Leu Gly Leu Leu Gln Glu Leu Asp Leu Ser 275 280 285

Gly Ser Ser Leu Val Pro Leu Pro Glu Thr Leu Leu His His Leu Pro 290 295 300

Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Gln Cys Arg Arg Leu 305 310 315 320

Val Arg Glu Gly Ala Val His Arg Gln Pro Gly Ser Ser Pro Lys Val 325 330 335

Val Leu His Cys Gly Asp Thr Gln Glu Ser Ala Arg Gly Pro Asp Ile 340 345 350

Leu

<210> 3

<211> 2557

<212> DNA

<213> Homo sapiens

<220>
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<222> (14)..(1075)
<223>

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| 190                               | 195          | 200                               |           |              |            |      |
|-----------------------------------|--------------|-----------------------------------|-----------|--------------|------------|------|
|                                   |              | agc ctg gat<br>Ser Leu Asp<br>215 |           |              |            | 673  |
|                                   |              | ggg ctg gga<br>Gly Leu Gly<br>235 |           |              |            | 721  |
|                                   |              | cct gag ctg<br>Pro Glu Leu<br>250 |           |              |            | 769  |
|                                   |              | ctg gac ctg<br>Leu Asp Leu<br>265 |           |              |            | 817  |
|                                   |              | ttt tca ggc<br>Phe Ser Gly<br>280 |           |              |            | 865  |
|                                   |              | ctg gtg ccc<br>Leu Val Pro<br>295 |           |              |            | 913  |
|                                   |              | agc gtc agc<br>Ser Val Ser<br>315 |           |              |            | 961  |
|                                   |              | ggc acc tac<br>Gly Thr Tyr<br>330 |           |              |            | 1009 |
|                                   |              | tgc gta gac<br>Cys Val Asp<br>345 |           |              |            | 1057 |
| ggc ccc acc<br>Gly Pro Thr<br>350 |              | caaatggtgt                        | ggcccaggg | c cacataaca  | g 1105     | 5    |
| actgctgtcc                        | tgggctgcct c | aggtcccga gt                      | aacttatg  | ttcaatgtgc ( | caacaccagt | 1165 |
| ggggagcccg                        | caggcctatg t | ggcagcgtc ac                      | cacaggag  | ttgtgggcct a | aggagaggct | 1225 |
| ttggacctgg (                      | gagccacacc t | aggagcaaa gt                      | ctcacccc  | tttgtctacg ( | ttgcttcccc | 1285 |
| aaaccatgag (                      | cagagggact t | cgatgccaa ac                      | cagactcg  | ggtcccctcc   | tgcttccctt | 1345 |
| cccacttat                         | ccccaagtg c  | cttccctca tg                      | cctgggcc  | ggctgacccg ( | caatgggcag | 1405 |
|                                   |              | cagggcaga gt                      |           |              |            | 1465 |
|                                   |              | ggggcgagt tt                      |           |              |            | 1525 |
|                                   |              | atccttttc ta                      |           |              |            | 1585 |
| attgcaaaga a                      | atcaagtcca c | ccttctcat gt                      | gacagatg  | gggaaactga ( | ggccttgaga | 1645 |

| aggaaaaagg | ctaatctaag               | ttcctgcggg | cagtggcatg | actggagcac | agcctcctgc | 1705         |
|------------|--------------------------|------------|------------|------------|------------|--------------|
| ctcccagccc | ggacccaatg               | cactttcttg | tctcctctaa | taagccccac | cctccccgcc | 1765         |
| tgggctcccc | ttgctgccct               | tgcctgttcc | ccattagcac | aggagtagca | gcagcaggac | 1825         |
| aggcaagagc | ctcacaagtg               | ggactctggg | cctctgacca | gctgtgcggc | atgggctaag | 1885         |
| _          | cttcggagcc<br>ggttggggtc |            |            |            |            | 1945<br>2005 |
| gcatcctcta | gatgctgccc               | caaggagttg | ctgcagttct | ggagcctcat | ctggctggga | 2065         |
| tctccaaggg | gcctcctgga               | ttcagtcccc | actggccctg | agcacgacag | cccttcttac | 2125         |
| cctcccagga | atgccgtgaa               | aggagacaag | gtctgcccga | cccatgtcta | tgctctaccc | 2185         |
| cagggtagca | tctcagcttc               | cgaaccctgg | gctgtttcct | tagtcttcat | tttataaaag | 2245         |
| ttgttgcctt | tttaacggag               | tgtcactttc | aaccggcctc | ccctacccct | gctggccggg | 2305         |
| gatggagaca | tgtcatttgt               | aaaagcagaa | aaaggttgca | tttgttcact | tttgtaatat | 2365         |
| tgtcctgggc | ctgtgttggg               | gtgttggggg | aagctgggca | tcagtggcca | catgggcatc | 2425         |
| aggggctggc | cccacagaga               | ccccacaggg | cagtgagete | tgtcttcccc | cacctgccta | 2485         |
| gcccatcatc | tatctaaccg               | gtccttgatt | taataaacac | tataaaaagt | taaaaaaaaa | 2545         |
| aaaaaaaaa  | aa                       |            | 255        | 57         |            |              |

<210> 4

<211> 353

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (121)..(121)

<223> 'Xaa' in position 121 represents Ala or Thr.

<400> 4

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Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr Phe Gly 20 25 30

- Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser Gly Leu Gly 35 40 45
- Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu Asp 50 55 60
- Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu Ser Val Leu Ala Gly 65 70 75 80
- Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu Leu 85 90 95
- Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu Ser 100 105 110
- Leu Asp Leu Ser His Asn Gly Leu Xaa Ala Leu Pro Ala Glu Ser Phe 115 120 125
- Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser His Asn Gln Leu Arg 130 135 140
- Glu Val Ser Val Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala Leu 145 .150 155 160
- His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Val Pro His Pro 165 170 175
- Thr Arg Ala Gly Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala 180 185 190
- Trp Asn Arg Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg 195 200 205
- Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala 210 215 220
- Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln 225 230 235 240
- Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly Leu 245 250 255
- Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala Gly Ala 260 265 270
- Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp Leu Ser Gly

8

275 280 285 Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu His Leu Pro Ala 295 300 Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys Arg Arg Leu Val 315 Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser Pro Lys Val Ala 330 335 Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg Gly Pro Thr Ile 345 Leu <210> 5 <211> 25 <212> DNA <213> Artificial : primer <400> 5 25 attaaccctc actaaatgct gggtg <210> 6 <211> 31 <212> DNA <213> Artificial : primer <400> 6 31 cattatgctg agtgatatct tttttttt g <210> 7 <211> 22 <212> DNA

<400> 7 acgcggggg gtcgcctagg tg

<213> Artificial : primer

1

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<210> 8
<211> 29
<212> DNA
<213> Artificial : primer
<400> 8
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